

RESULT 6

US-10-367-057-53

; Sequence 53, Application US/10367057
 ; Publication No. US20050100554A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cuthill, Scott;
 ; APPLICANT: Jackson, Amanda;
 ; APPLICANT: Lewin, David A.;
 ; APPLICANT: Ooi, Chean Eng
 ; TITLE OF INVENTION: Complexes and Methods of Using Same
 ; FILE REFERENCE: 21402-559
 ; CURRENT APPLICATION NUMBER: US/10/367,057
 ; CURRENT FILING DATE: 2003-02-14
 ; PRIOR APPLICATION NUMBER: 60/256,911
 ; PRIOR FILING DATE: 2002-02-14
 ; NUMBER OF SEQ ID NOS: 198
 ; SOFTWARE: CuraSeqList version 0.1
 ; SEQ ID NO 53
 ; LENGTH: 958
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-367-057-53

Query Match 100.0%; Score 82; DB 5; Length 958;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQSLGSRGRSSLSLAK 18
 |||||
 Db 104 RQSLGSRGRSSLSLAK 121

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1	"20050100554"	US-PGPUB; USPAT	OR	ON	2006/10/20 14:02
L2	1	L1 and antibod\$	US-PGPUB; USPAT	OR	ON	2006/10/20 14:04
L3	4	GEF-H1 near antibod\$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/10/20 15:09
L4	4	(GEF-H1 or ARHGEF2) near antibod\$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/10/20 15:11
L5	22	(GEF-H1 or ARHGEF2) and antibod\$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/10/20 15:12
L6	27	GEF-H1 or ARHGEF2	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/10/20 15:13

d his

(FILE 'HOME' ENTERED AT 17:05:10 ON 20 OCT 2006)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 17:05:29 ON 20 OCT 2006

L1 9 S (GEF-H1 OR GEFH1 OR ARHGEF2) AND ANTIBOD?
L2 80 S GEF-H1 OR GEFH1 OR ARHGEF2
L3 9 DUP REM L1 (0 DUPLICATES REMOVED)
L4 41 DUP REM L2 (39 DUPLICATES REMOVED)
L5 97 S SMEAL T R/AU OR CALLOW M G/AU OR JALLAL B/AU
L6 44 DUP REM L5 (53 DUPLICATES REMOVED)
L7 1 S L2 AND L6

=>

SCORE Search Results Details for Application 10611671 and Search Result us-10-611-671-4.rapbm

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OM protein - protein search, using sw model

Run on: September 19, 2006, 23:22:28 ; Search time 182 Seconds
(without alignments)
45.812 Million cell updates/sec

Title: US-10-611-671-4
Perfect score: 82
Sequence: 1 RQSLLGSRGRSSLAK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	82	100.0	18	4	US-10-611-671-4
2	82	100.0	19	4	US-10-611-671-8
3	82	100.0	19	4	US-10-611-671-9

4	82	100.0	46	4	US-10-611-671-49	Sequence 49, Appl
5	82	100.0	920	4	US-10-611-671-2	Sequence 2, Appli
6	82	100.0	958	5	US-10-367-057-53	Sequence 53, Appl
7	82	100.0	994	5	US-10-723-860-2066	Sequence 2066, Ap
8	54	65.9	18	4	US-10-611-671-47	Sequence 47, Appl
9	50	61.0	85	4	US-10-425-115-245626	Sequence 245626,
10	45	54.9	69	4	US-10-425-115-225403	Sequence 225403,
11	43	52.4	140	4	US-10-425-115-333843	Sequence 333843,
12	43	52.4	264	6	US-11-096-568A-25037	Sequence 25037, A
13	43	52.4	285	6	US-11-096-568A-25036	Sequence 25036, A
14	43	52.4	2360	4	US-10-437-963-187801	Sequence 187801,
15	42	51.2	69	4	US-10-437-963-129723	Sequence 129723,
16	42	51.2	681	4	US-10-437-963-195028	Sequence 195028,
17	41	50.0	53	3	US-09-864-408A-7878	Sequence 7878, Ap
18	41	50.0	163	4	US-10-437-963-161912	Sequence 161912,
19	41	50.0	188	5	US-10-467-657-3200	Sequence 3200, Ap
20	41	50.0	197	4	US-10-437-963-165251	Sequence 165251,
21	41	50.0	205	4	US-10-335-977-5888	Sequence 5888, Ap
22	41	50.0	297	4	US-10-425-115-351232	Sequence 351232,
23	41	50.0	303	4	US-10-335-977-5889	Sequence 5889, Ap
24	41	50.0	310	4	US-10-335-977-5890	Sequence 5890, Ap
25	41	50.0	361	4	US-10-425-114-51048	Sequence 51048, A
26	41	50.0	695	4	US-10-156-761-13358	Sequence 13358, A
27	41	50.0	796	3	US-09-801-368-30	Sequence 30, Appl
28	41	50.0	797	6	US-11-097-143-21042	Sequence 21042, A
29	41	50.0	1522	4	US-10-437-963-175194	Sequence 175194,
30	40	48.8	18	4	US-10-211-088-35	Sequence 35, Appl
31	40	48.8	96	4	US-10-425-115-311936	Sequence 311936,
32	40	48.8	122	4	US-10-425-115-306244	Sequence 306244,
33	40	48.8	123	4	US-10-437-963-163757	Sequence 163757,
34	40	48.8	139	6	US-11-096-568A-1451	Sequence 1451, Ap
35	40	48.8	150	4	US-10-425-115-268317	Sequence 268317,
36	40	48.8	160	4	US-10-744-149-14	Sequence 14, Appl
37	40	48.8	160	5	US-10-744-620-14	Sequence 14, Appl
38	40	48.8	160	6	US-11-096-568A-1450	Sequence 1450, Ap
39	40	48.8	210	6	US-11-096-568A-23933	Sequence 23933, A
40	40	48.8	244	4	US-10-437-963-168353	Sequence 168353,
41	40	48.8	247	6	US-11-096-568A-23932	Sequence 23932, A
42	40	48.8	248	4	US-10-425-115-300754	Sequence 300754,
43	40	48.8	249	4	US-10-425-114-57244	Sequence 57244, A
44	40	48.8	262	4	US-10-180-375-136	Sequence 136, App
45	40	48.8	262	4	US-10-183-687-266	Sequence 266, App
46	40	48.8	262	4	US-10-425-115-233343	Sequence 233343,
47	40	48.8	270	4	US-10-425-114-69441	Sequence 69441, A
48	40	48.8	563	4	US-10-639-720A-2	Sequence 2, Appli
49	40	48.8	563	4	US-10-704-332-7	Sequence 7, Appli
50	40	48.8	563	4	US-10-704-332-9	Sequence 9, Appli
51	40	48.8	563	4	US-10-704-332-11	Sequence 11, Appl
52	40	48.8	563	4	US-10-704-332-14	Sequence 14, Appl
53	40	48.8	564	4	US-10-704-332-18	Sequence 18, Appl
54	40	48.8	698	4	US-10-437-963-156597	Sequence 156597,
55	40	48.8	712	4	US-10-437-963-112121	Sequence 112121,
56	40	48.8	746	4	US-10-425-114-64987	Sequence 64987, A
57	39.5	48.2	1494	4	US-10-437-963-194014	Sequence 194014,
58	39	47.6	78	4	US-10-767-701-47752	Sequence 47752, A
59	39	47.6	84	4	US-10-425-115-249302	Sequence 249302,
60	39	47.6	86	4	US-10-425-115-256239	Sequence 256239,
61	39	47.6	86	4	US-10-425-115-356540	Sequence 356540,
62	39	47.6	89	4	US-10-437-963-188270	Sequence 188270,
63	39	47.6	103	4	US-10-425-115-205500	Sequence 205500,
64	39	47.6	107	4	US-10-425-115-292377	Sequence 292377,

SCORE Search Results Details for Application 10611671 and Search Result us-10-611-671-4.rapbn.

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OM protein - protein search, using sw model

Run on: September 19, 2006, 23:23:43 ; Search time 32 Seconds
(without alignments)
39.739 Million cell updates/sec

Title: US-10-611-671-4
Perfect score: 82
Sequence: 1 RQSLLGSRGRSSLSLAK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 256596 seqs, 70647373 residues

Total number of hits satisfying chosen parameters: 256596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
1	40	48.8	139	6	US-10-953-349-39556	Sequence 39556, A
2	40	48.8	160	6	US-10-953-349-39555	Sequence 39555, A
3	40	48.8	210	7	US-11-056-355B-17985	Sequence 17985, A
4	40	48.8	244	6	US-10-449-902-50983	Sequence 50983, A
5	40	48.8	247	7	US-11-056-355B-17984	Sequence 17984, A
6	40	48.8	540	6	US-10-449-902-45649	Sequence 45649, A
7	40	48.8	1115	7	US-11-056-355B-78536	Sequence 78536, A
8	40	48.8	1121	7	US-11-056-355B-78535	Sequence 78535, A
9	40	48.8	1181	7	US-11-056-355B-49997	Sequence 49997, A
10	40	48.8	1187	7	US-11-056-355B-49996	Sequence 49996, A
11	40	48.8	1191	7	US-11-056-355B-78534	Sequence 78534, A
12	40	48.8	1257	7	US-11-056-355B-49995	Sequence 49995, A
13	39	47.6	200	7	US-11-056-355B-65451	Sequence 65451, A
14	39	47.6	256	6	US-10-449-902-39280	Sequence 39280, A
15	39	47.6	257	6	US-10-953-349-2510	Sequence 2510, Ap
16	39	47.6	257	7	US-11-056-355B-38462	Sequence 38462, A
17	39	47.6	257	7	US-11-056-355B-105972	Sequence 105972,
18	39	47.6	257	7	US-11-056-355B-117211	Sequence 117211,
19	39	47.6	264	6	US-10-953-349-2509	Sequence 2509, Ap
20	39	47.6	264	7	US-11-056-355B-38461	Sequence 38461, A
21	39	47.6	264	7	US-11-056-355B-105971	Sequence 105971,
22	39	47.6	264	7	US-11-056-355B-117210	Sequence 117210,
23	39	47.6	271	6	US-10-449-902-32465	Sequence 32465, A
24	39	47.6	272	6	US-10-953-349-11616	Sequence 11616, A
25	39	47.6	299	7	US-11-056-355B-105970	Sequence 105970,
26	39	47.6	299	7	US-11-056-355B-117209	Sequence 117209,
27	39	47.6	301	6	US-10-449-902-56312	Sequence 56312, A
28	39	47.6	380	7	US-11-056-355B-20182	Sequence 20182, A
29	39	47.6	391	7	US-11-056-355B-20181	Sequence 20181, A
30	39	47.6	432	6	US-10-449-902-48478	Sequence 48478, A
31	38	46.3	258	6	US-10-953-349-26872	Sequence 26872, A
32	38	46.3	277	7	US-11-056-355B-82606	Sequence 82606, A
33	38	46.3	403	7	US-11-330-403-2526	Sequence 2526, Ap
34	38	46.3	403	7	US-11-330-403-16284	Sequence 16284, A
35	38	46.3	433	6	US-10-953-349-26871	Sequence 26871, A
36	38	46.3	789	6	US-10-449-902-46564	Sequence 46564, A
37	38	46.3	789	6	US-10-449-902-48999	Sequence 48999, A
38	38	46.3	1536	7	US-11-330-403-1325	Sequence 1325, Ap
39	37	45.1	72	6	US-10-449-902-44527	Sequence 44527, A
40	37	45.1	113	7	US-11-056-355B-13716	Sequence 13716, A
41	37	45.1	114	7	US-11-293-697-4571	Sequence 4571, Ap
42	37	45.1	151	7	US-11-056-355B-13713	Sequence 13713, A
43	37	45.1	392	7	US-11-330-403-7739	Sequence 7739, Ap
44	37	45.1	402	7	US-11-330-403-6636	Sequence 6636, Ap
45	37	45.1	406	7	US-11-330-403-5333	Sequence 5333, Ap
46	37	45.1	434	7	US-11-221-332-94	Sequence 94, Appl
47	37	45.1	602	7	US-11-056-355B-88014	Sequence 88014, A
48	37	45.1	604	7	US-11-056-355B-88013	Sequence 88013, A
49	37	45.1	639	7	US-11-056-355B-88012	Sequence 88012, A
50	37	45.1	644	7	US-11-056-355B-71272	Sequence 71272, A
51	37	45.1	679	7	US-11-056-355B-71271	Sequence 71271, A
52	37	45.1	686	7	US-11-030-653-22	Sequence 22, Appl
53	37	45.1	752	7	US-11-056-355B-71270	Sequence 71270, A
54	36	43.9	134	6	US-10-449-902-51228	Sequence 51228, A
55	36	43.9	142	6	US-10-449-902-55870	Sequence 55870, A
56	36	43.9	187	6	US-10-953-349-6691	Sequence 6691, Ap
57	36	43.9	188	6	US-10-953-349-8410	Sequence 8410, Ap
58	36	43.9	197	6	US-10-953-349-6690	Sequence 6690, Ap
59	36	43.9	201	7	US-11-056-355B-24263	Sequence 24263, A

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This page gives you Search Results detail for the Application 10611671 and Search Result us-10-6:
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OM protein - protein search, using sw model

Run on: September 19, 2006, 23:17:18 ; Search time 39 Seconds
(without alignments)
44.408 Million cell updates/sec

Title: US-10-611-671-4
Perfect score: 82
Sequence: 1 RQSLGSRGRSSLSLAK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	75	91.5	573	2 I49342	hypothetical oncog
2	43	52.4	405	2 AI3232	replication protei
3	42	51.2	86	2 E64003	hypothetical prote
4	41	50.0	188	2 G81155	hypothetical prote
5	41	50.0	188	2 H81949	hypothetical prote
6	41	50.0	250	2 T14546	beta-fructofuranos
7	41	50.0	796	1 A32434	abaA protein - Eme
8	40	48.8	414	2 C89428	protein T08D2.7 [i

Comments /
Suggestions

5	82	100.0	985	2	Q8TDA3_HUMAN	Q8tda3	homo sapien
6	82	100.0	986	2	Q5VY92_HUMAN	Q5vy92	homo sapien
7	82	100.0	986	2	Q865S3_CANFA	Q865s3	canis famil
8	82	100.0	987	2	Q5VY93_HUMAN	Q5vy93	homo sapien
9	75	91.5	596	1	ARHG2_MOUSE	Q60875	mus musculu
10	75	91.5	637	2	Q3TYZ4_MOUSE	Q3tyz4	mus musculu
11	75	91.5	956	2	Q3TBI4_MOUSE	Q3tbi4	mus musculu
12	75	91.5	958	2	Q3TJ16_MOUSE	Q3tj16	mus musculu
13	75	91.5	985	2	Q5FVC2_RAT	Q5fvc2	rattus norv
14	75	91.5	985	2	Q8CHE1_MOUSE	Q8che1	mus musculu
15	75	91.5	985	2	Q923E0_MOUSE	Q923e0	mus musculu
16	75	91.5	985	2	Q9ESG7_MOUSE	Q9esg7	mus musculu
17	72	87.8	98	2	Q9W736_XENLA	Q9w736	xenopus lae
18	72	87.8	967	2	Q6INN2_XENLA	Q6inn2	xenopus lae
19	72	87.8	976	2	Q6AX47_XENLA	Q6ax47	xenopus lae
20	69	84.1	978	2	Q6NY14_XENTR	Q6ny14	xenopus tro
21	69	84.1	1129	2	Q4SWE0_TETNG	Q4swe0	tetraodon n
22	62	75.6	279	2	Q4RAP6_TETNG	Q4rap6	tetraodon n
23	49	59.8	187	2	Q5DGZ3_SCHJA	Q5dgz3	schistosoma
24	48	58.5	483	1	CIMA_METAC	Q8tjj1	methanosarc
25	48	58.5	483	1	CIMA_METMA	P58966	methanosarc
26	48	58.5	483	2	Q46FZ1_METBA	Q46fz1	methanosarc
27	45	54.9	268	2	Q2LR09_9DELT	Q2lr09	syntrophus
28	44	53.7	56	2	Q7UQY8_RHOBA	Q7uqy8	rhodopirell
29	44	53.7	162	2	Q396A1_BURS3	Q396a1	burkholderi
30	44	53.7	401	2	Q3STK5_NITWN	Q3stk5	nitrobacter
31	44	53.7	442	2	Q6FVR1_CANGA	Q6fvr1	candida gla
32	44	53.7	485	2	Q41Q17_METBU	Q41q17	methanococc
33	43.5	53.0	694	2	Q56JK9_APIME	Q56jk9	apis mellif
34	43	52.4	158	2	Q54BV1_DICDI	Q54bv1	dictyosteli
35	43	52.4	164	2	Q72A69_DESVH	Q72a69	desulfovibr
36	43	52.4	405	2	Q66165_9RHI2	Q66165	agrobacteri
37	43	52.4	405	2	Q8U691_AGRIT5	Q8u691	agrobacteri
38	43	52.4	411	2	Q7D2P0_AGRIT5	Q7d2p0	agrobacteri
39	43	52.4	483	2	Q8ZT56_PYRAE	Q8zt56	pyrobaculum
40	43	52.4	656	2	Q2JUF7_9CYAN	Q2juf7	cyanobacter
41	43	52.4	758	2	Q6BZ53_DEBHA	Q6bz53	debaryomyce
42	43	52.4	1399	2	Q4PBD7_USTMA	Q4pbd7	ustilago ma
43	43	52.4	2013	2	Q4UAG2_THEAN	Q4uag2	theileria a
44	43	52.4	2825	2	Q6EUI5_ORYSA	Q6eui5	oryza sativ
45	42.5	51.8	290	2	Q5B6D9_EMENI	Q5b6d9	aspergillus
46	42	51.2	76	2	Q6K5X0_ORYSA	Q6k5x0	oryza sativ
47	42	51.2	86	1	Y173_HAEIN	P43960	haemophilus
48	42	51.2	262	2	Q3AY18_SYNS9	Q3ay18	synechococc
49	42	51.2	285	2	Q7U6M3_SYNXP	Q7u6m3	synechococc
50	42	51.2	335	2	Q4RN31_TETNG	Q4rn31	tetraodon n
51	42	51.2	373	2	Q6LRV3_PHOPR	Q6lr31	photobacter
52	42	51.2	399	2	Q8GVC7_PHYIN	Q8gvc7	phytophthor
53	42	51.2	411	2	Q3W7X0_9ACTO	Q3w7x0	frankia sp.
54	42	51.2	606	2	Q7S6R5_NEUCR	Q7s6r5	neurospora
55	42	51.2	1203	2	Q4P9D2_USTMA	Q4p9d2	ustilago ma
56	42	51.2	1572	2	Q4D1E2_TRYCR	Q4d1e2	trypanosoma
57	42	51.2	1572	2	Q4DUN0_TRYCR	Q4dun0	trypanosoma
58	41.5	50.6	189	2	Q3G1G5_9DELT	Q3g1g5	pelobacter
59	41	50.0	63	2	Q8VNR2_ECOLI	Q8vnr2	escherichia
60	41	50.0	106	2	Q8KL53_RHIET	Q8kl53	rhizobium e
61	41	50.0	188	2	Q5F9K2_NEIG1	Q5f9k2	neisseria g
62	41	50.0	188	2	Q9JV31_NEIMA	Q9jv31	neisseria m
63	41	50.0	188	2	Q9K019_NEIMB	Q9k019	neisseria m
64	41	50.0	228	2	Q4TGG5_TETNG	Q4tgg5	tetraodon n
65	41	50.0	250	2	Q42646_BETVU	Q42646	beta vulgar

SCORE Search Results Details for Application 10611671 and Search Result us-10-611-671-4.1

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OM protein - protein search, using sw model

Run on: September 19, 2006, 23:22:18 ; Search time 51 Seconds
(without alignments)
30.893 Million cell updates/sec

Title: US-10-611-671-4
Perfect score: 82
Sequence: 1 RQSLGSRGRSSLSLAK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	43	52.4	534	2	US-09-252-991A-32086 Sequence 32086, A
2	42	51.2	774	2	US-09-252-991A-29669 Sequence 29669, A

SCORE Search Results Details for Application 10611671 and Search Result us-10-611-671-4.rag.

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OM protein - protein search, using sw model

```
Run on:      September 19, 2006, 23:12:23 ; Search time 197 Seconds
              (without alignments)
              41.776 Million cell updates/sec
```

Title: US-10-611-671-4
Perfect score: 82
Sequence: 1 RQSLGSRGRSSLSLAK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries

```

```
Database :      A_Geneseq_8:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	100.0	18	8	ADI34764	Adi34764 Human GEF
2	82	100.0	19	8	ADI34769	Adi34769 GEF-H1S K
3	82	100.0	19	8	ADI34768	Adi34768 GEF-H1S K
4	82	100.0	920	8	ADI34762	Adi34762 Human GEF
5	82	100.0	948	8	ABM83436	Abm83436 Human dia
6	82	100.0	958	7	ADF09552	Adf09552 Human rho
7	82	100.0	958	8	ABM83443	Abm83443 Human dia
8	82	100.0	969	8	ABM83440	Abm83440 Human dia
9	82	100.0	969	8	ABM83439	Abm83439 Human dia
10	82	100.0	969	8	ABM83441	Abm83441 Human dia
11	82	100.0	972	8	ABM83442	Abm83442 Human dia
12	82	100.0	985	8	ADS88428	Ads88428 Human pro
13	82	100.0	994	8	ADQ19247	Adq19247 Human sof
14	82	100.0	995	8	ABM83438	Abm83438 Human dia
15	82	100.0	996	8	ABM83437	Abm83437 Human dia
16	43	52.4	79	4	AAU62434	Aau62434 Propionib
17	43	52.4	79	6	ABM58953	Abm58953 Propionib
18	43	52.4	534	7	ABO83340	Abo83340 Pseudomon
19	42	51.2	72	5	ABP09181	Abp09181 Human ORF
20	42	51.2	399	7	ABB80244	Abb80244 P. infest
21	42	51.2	774	7	ABO80923	Abo80923 Pseudomon
22	41	50.0	53	5	ABP34966	Abp34966 Human ORF
23	41	50.0	65	3	AAG57071	Aag57071 Arabidops
24	41	50.0	188	3	AAY75226	Aay75226 Neisseria
25	41	50.0	188	3	AAY75228	Aay75228 Neisseria
26	41	50.0	188	3	AAY75227	Aay75227 Neisseria
27	41	50.0	188	6	ABP78335	Abp78335 N. gonorr
28	41	50.0	188	9	AEB19124	Aeb19124 Neisseria
29	41	50.0	200	7	ABO74829	Abo74829 Pseudomon
30	41	50.0	205	2	AAW20158	Aaw20158 H. pylori
31	41	50.0	310	2	AAW20871	Aaw20871 H. pylori
32	41	50.0	361	8	ADX88384	Adx88384 Plant ful
33	41	50.0	419	7	ABO79741	Abo79741 Pseudomon
34	41	50.0	797	4	ABB64750	Abb64750 Drosophil
35	41	50.0	812	2	AAR10047	Aar10047 abaA gene
36	40	48.8	133	7	ABO77465	Abo77465 Pseudomon
37	40	48.8	160	3	AAY96218	Aay96218 Maize LEC
38	40	48.8	182	2	AAY73936	Aay73936 Human pro
39	40	48.8	249	8	ADX94580	Adx94580 Plant ful
40	40	48.8	262	6	ABR40723	Abr40723 Zea mays
41	40	48.8	262	7	ADC23631	Adc23631 Polypepti
42	40	48.8	270	8	ADY13626	Ady13626 Plant ful
43	40	48.8	563	8	ADK71105	Adk71105 Human aci
44	40	48.8	563	8	ADP43823	Adp43823 Human CB1
45	40	48.8	563	8	ADP43825	Adp43825 Human FB4
46	40	48.8	563	8	ADP43830	Adp43830 Human aci
47	40	48.8	563	8	ADP43827	Adp43827 Human SC2
48	40	48.8	564	8	ADP43834	Adp43834 Human SC2
49	40	48.8	746	8	ADY09172	Ady09172 Plant ful
50	40	48.8	769	9	ABM97417	Abm97417 M. xanthu
51	40	48.8	860	8	ADI28828	Adi28828 Human mod
52	40	48.8	908	5	ABB97232	Abb97232 Novel hum
53	40	48.8	1257	8	ADU20533	Adu20533 A. thalia
54	40	48.8	1257	8	ADU20384	Adu20384 A. thalia
55	39	47.6	18	7	ADC22186	Adc22186 Protein b
56	39	47.6	64	7	ABM89344	Abm89344 Rice abio
57	39	47.6	165	8	ADX74951	Adx74951 Plant ful